



```

Db 79 TDPDNGDNNQLTQ-----AQKTAAGFEVW-----GKIRDTSPKN-D 115
Qy 64 PDSSSE--YRWYG--YESYVRGHP-----YKQFRAHDLRVNL 98
Db 116 PDTSNDLVQOMOGKLVGIDAHRPDGI GTGKNLRQPTIANDIKPLTFKFPALSDLHDS 175
Qy 99 EGSRSYQVYCFNLKAFPLGSDSSVKK--WYKHHDSITKFEDYAMSP-----RIT 147
Db 176 ERRR-FDPKRLNTIKYGYGNLTTPSKNNMTYINHQAADKKNNKPPDPENIRFGYLEQ 234
Qy 148 GDELNOK-----LRAVYNGHPONANGIMEGLEPLN-----178
Db 235 GSSLTQKNADTPNDKDRIPKPMPILEFHG--ENASSQLPSAGKFNVTGMWLYLSDVKRP 292
Qy 179 AIRVTOEAVWYSDNAPISNPDESFRRESNLYSTQSL-----219
Db 293 ALSASDRVGVYILNAGSKS-----EGDVVSAHITYLNGFOYKHPATYQVDPDTN 343
Qy 220 -MRQALKOLIDPMLATKMKQVDPDF-----QLSIFESQK--GDKYNGKYONLISG 269
Db 344 SLTGKLSYDNPQOQAQGYIKSQPDTTKKYNETDVIQIDAKINGNRFRVGTAKSLVNN 403
Qy 270 L-----VPTKPPGDPMPMPNPQOTTSVLIRKYYAIGDYSKLLGATLQLTGDNVNS 321
Db 404 TETAPFIKELFSKKANPNP--NPN-----SDTLEGGFYESGDEL--442
Qy 322 FQARVSSND-----IGERIELSDGTYYLTTELNSPAGYSIAEPIITFKYKAGVYTIIDG 375
Db 443 --AGKFLSNDNASYVFGGKRDTDKPVATKTYVESAGE--KPSTSFVDNETIGRLINS 498
Qy 376 KOIENPNKEIVE--PYSVEAYNDF-----BEFSVLTON-----YAKFYAK 415
Db 499 KRLNDVANEKIDNGDIPTSDERYDEFPWGEKKAETFKVYSSQVAPAYEGQDKRYE--556
Qy 416 NKNSSQVYVYCFNADIKSPDSEDGKTMPTDTTGEV-----453
Db 557 --NGNYDLSASSVDKLADADAVKANOSIKEYPNATLNKDNQVTAIYLOEAKDNKPYTA 614
Qy 454 ----KTHIA-GRDLF-----KYTVKPRDTPDTFLKHIKVYI-----486
Db 615 IRAKSTQHSIFGELTYLNDANQOTRSTFYOGGADSTLTPKAGKTYTNGNAGYLOK 674
Qy 487 EKGYREKGAIEYSG-----LLETQLRATQLAIIYFT-----DSAEIDKDKLDYHGF 535
Db 675 DKYSNNEETIKKKHQDYLTFED-----FTPEDDDDDLTASDDSDDDAHG 722
Qy 536 GDMNDSTLAVAKLIVYADSNRPQTLDDFTIPNNKTYQSLIGTQMHPELDVITIMED 595
Db 723 DDL-----IASDSDDDADGDDSDDL--GDGADDAAGKYVHAGN--IRPEP 767
Qy 596 KKEVIVP--THNLTL-----RKTVTGLAGDRTKDPHFETELKNNKOELL 637
Db 768 ENKYLINETHETKTAALOGKNAKAFVDVDTNLSLTKLNDENGDIYFDL--KNGKIDGT 835
Qy 638 SQTVAKTDKTNLEFKDKATINLKHGSLTLOGLPEGYSYLKETESEGKVKVNSOEVA--696
Db 826 GFYAKADVNYREVG--NNQGG-----GFLVNIKIDVKGQGFNGESELG 871
Qy 697 -----NATVSKTG-----ITSDETLAFENNEKPPVPTGVOKINGYL--ALIVYA 739
Db 872 QLOYDKGDIINDYAEKAGAVFGAVKDKMSKITKQTPSVHTWTHRLMLAIKALFVGA 931
Qy 740 GISLIGM 746
Db 932 VLEPLSYW 938

```

```

RESULT 2
US-08-867-941-11
; Sequence 11, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M

```

```

; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Qui-jun
; APPLICANT: Yang, Yan-ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELEPHONE: (416) 595-1153
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-867-941-11
;
Query Match 4.5%; Score 178; DB 2; Length 898;
Best local similarity 18.6%; Pred. No. 4.9e-06;
Matches 171; Conservative 118; Mismatches 305; Indels 324; Gaps 42;

```

[illegible]

RESULT 3  
 US-09-074-658-70  
 Sequence 70, Application US/09074658  
 Patent No. 6184371  
 GENERAL INFORMATION:  
 APPLICANT: Loosmore, Sheena, M  
 APPLICANT: Run-Pan Du  
 APPLICANT: Qunjun Wang  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Klein, Michel H  
 TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 NUMBER OF SEQUENCES: 78  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Slim & McBurey  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074,658  
 FILING DATE: 08-May-1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-795  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 905 amino acids  
 TYPE: amino acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-70

```

Query Match	4.5%;	Score 176;	DB 4;	Length 905;
Best Local Similarity	20.6%;	Pred. No. 7.2e-06;		
Matches 164;	Conservative 102;	Mismatches 264;	Indels 266;	Gaps 40;

QY	84	YKFOEVAHDDRVMLDESSRSYQVYCFNLKKA-----EPPLSDSSVVK-----WYKHDGI	133
Db	165	YFDXFPKISDL--HLENSE-----HYFPAKKANNTKIYIGALSSPANKPYMYMQOQNI	218
QY	134	STR--FEDYA-----MSPRIT-----GDELNOKLRAVMYNG-----HPQMANIMEGL	174
Db	219	KNKKRGDDYQNIREFGYMELRELDLNKKGADNQSDKNRAIIFFTPPLEYHEGNASTHLP--	276
QY	175	EPLMAIRYTOCAWVYYSQDNP-----ISNPDE-----SPKRESESLVSTQSLSL----	219
Db	277	---KAGKDYEGNMLYLTIDVKKRPFLKTDKQVGTYNSTFKSMEGVLVSAAHYLMSFK	333
QY	220	-----MROALKQIDENLTKMFKQVDPDF-----QLSIESEDK--	254
Db	334	YKHHPATYSDVFDQNTLKGKLSYDNDNNKQJADRSYIRSGEDDDKYNNEADYELDAKIN	393
QY	255	GDKTKNGKQNLSSGL-----VPRKPPYGGPPMPMPNPPOPTSVLIRKVAIGDYSKL	306
Db	394	GNRFTTAKSLIDNTNTAPVKELFSKAKPNPN--DPN-----SDT	434
QY	307	LEGATLQLTGNGVNSPQARVSSNDI-----GERIELSDGYTTELMSPAGSYAEP	359
Db	435	LEGGFYSGSGDEL---AGKFLSDNNAITFYVFGKKRDKTTEPAVKIYVS--TGFE--KP	487
QY	360	ITTFVEAKQVYTLIDGK---QIENPNKEIPEYSEVAYNDF-----EEFSVLT	405
Db	488	STSPFNGNEIGSIIIDGKLNDEVANNQJIEDETVPVSNKEYYEYNGRPNKOFTKKNASVQ	547
QY	406	QNTA-----KFTY-----AR--KNKSSQVYVCFMADLKSPPESEGGKMTPTDFT	449
Db	548	KNPAYFGQHDKFYENGNYDLSAKENAKLGSQDTSNKSILAKYPA---KYSTDNKV	603
QY	450	T-----GEVKTHTIAGRDLEFYVTKPBDTPDPLK----	480
Db	604	TKIYLQAKDKPYTAIHAKSDHISFGEVLYLNDKKGAPTSYFYQGGQADVSYOLPSAGK	663
QY	481	-----HIKKVIEKGYRREKGOAIEYSGLTETQALRAATOLAIYPT-----	519
Db	664	FTYNGMLMAGYLTQKKDKGYSKDEDTIKQGLKD-----YLTQOFIPQDDDDDD	712
QY	520	DSAEIADKDKLD--YHGGGDAMDSTILAAKILVEYAQDSNPQLTDLDFPIPNNNKYSLI	578
Db	713	DSLTLASDSDODDNTNHGDDDL-----IASDSDSDDDDTDGDDSDDL--GGGADDDAA	761
QY	579	GTOVHPBEDLVIIIMEDKEVIYV--THNLTL-----RKYVGLIADRT	620
Db	762	GKYVTHAGN---IRPEENKILPIINEPTHETFPALDOKKNAKFPYVNDTSLGKLEDER	817
QY	621	KDFHEIELKNNKQELLISQVTKYTDKTLNEFDKQKATINLKHGESLTLQGLPEGYSYLVE	660
Db	818	GDIYFEDI--KNGKIDGIGFTAKADVPVYREEVG---NNQGG-----GLYWIKD	861
QY	681	TDSEGYKAKVNASQEVA	696
Db	862	IDVKGREGFTNGEELA	877

RESULT 4  
US-09-074-658-15  
: Sequence 15, Application US/09074658  
: Patent No. 6184371  
: GENERAL INFORMATION:  
: APPLICANT: Loomore, Sheena M  
: APPLICANT: Run-Pan Du

```

APPLICANT: Qutjun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Slim & McBurney
STREET: 6th floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-15

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Query Match      3.9%; Score 154.5; DB 4; Length 2432;
Best Local Similarity 19.6%; Pred. No. 0.002;
Matches 169; Conservative 101; Mismatches 306; Indels 285; Gaps 41;

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QY 84 YKQFVADLRVNLDEGSSYOVYCFNLKAPLGL--SDSSVKKWKKKHGDIKTEDEDA 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 YFKFPALSDLHLDESRHR-FDPOKINTIKVGYGNLTTPSSNNTIINIQADNKKNNKP 219
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 142 MSP-----RITGDELNOK-----LRAVMNGHONANGIMEGLEPLN 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 220 VDPYENIRRGYLELQSSSLQKNADNONEDRIKPPMPLIFTHG--ENASSQLPSAKFN 277
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 -----AIRVTOEAVWYSDNAPISNPDESFKRESNINVTSQLSMRQA 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 278 YTCNMVLYLSDVKRRPALSDERIVGLYLNASGAN-----EDDVYSAHIHLYNGFQ 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 LKQLDPLNLTAKMPKQVPDF-----QLSIESEDKGDKYNGK----- 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 YKH-----TPATYVDEFTNSLTGKLSYDNPNO--QNNKGEYLKSOFTTKKVNED 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 -YQ-----NLSG--GLVPTKPPTPG-----DPPMPNPQPTTSVLRKYYAIGDVS 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 380 VYQIDAKINGNRFVGTAKSLVNEKTQAPFIKELFSKKNPNNPNP-----S 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 KLEGATLDTGDNVNSFOARVSSNDI-----SERIELSDGYTTLTLELNSPAGYSIA 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 428 DTLGEGFYGESGDEL-----AGKFLSDNDSYVYFGKROKTKTPVATKYTFYF-AGEF-- 480
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 358 EPIITFVEAGKYVTTIDGKIENP-NKEIVEPYSEAY-----NDFEESVLTQ-- 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 481 KPETSPVDNETIGIIRKGLNHNHINEDIIPSDDSYGYTGWCKPEKQFKKYSSSTQV 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 407 -----NYAFYYIAKNNKSSQVYVCYNADLAKSPDSEDGKTKTPDETIGEY----- 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 541 PAYFGHDKRYF--NGNYDLSASRVDKLADAVKANAKOSIKERYPNATLNKKNQVTA 596
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

QY 454 -----KYTHIA-GRDLF-----KYTVKPRDTPDPTFLKHKKV 485
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 597 IYLOEAKONKPYTAIRAKSYOHISFGETLYNDANOTPRRSYFVGGRADSTTLPOAGKF 656
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 486 I-----EKGYREKQALIEYSG-----LFEQLRAATQALAIYFF-----DS 521
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 657 TYNGIMAGYLTQKKKQKGYSDNAETIKKKGHPGYLLTEN-----FTPEDDDDL 704
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 AELDKDKLKYHGFQDMNDSTLAVAKILIVEYQDSNPOLDTDLDFIPNNKKYQSLIGTQ 581
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 705 TASDOSQDDNTHGGDDL-----IASDSDQDDDAOGDDSDDL--GDGADDDAAGKV 753
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 WHPEDLVDLIIRMEDKKEVIVP--THNLTL-----RKTYTGAGRTADF 623
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 754 YAGN-----IRPEFENKYLPINEPHEKTFALDGKNAKAFEVDFNTNSLTGKLNDERGDI 809
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 624 HFEIELKNNKQELLSTYVTKDNTNLEFKDKRTINLKHGESLTLGLPGYSYLVKETDS 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 810 VEDI--KNKRIGDTGFTADADVPNYREEVG--NNQGS-----GLYXINIKDIDV 853
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 684 EGYKVKVNSQEVY-----NATVSKTG-----ITSDETLAFENKKEVPVPTGVQD 727
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 854 KQFEGTNGEELAGOLHDKGQINDTAERKAGAVGAVKDKMSKITKTQTPSVHTMTTH 913
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 728 KINGYL--ALIVIAGISLGIW 746
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 914 RLNLAIKALFGVAVLPLSLW 934
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 5
US-08-447-031A-2
; Sequence 2, Application US/08447031A
; Patent No. 5851794

```

## GENERAL INFORMATION:

```

APPLICANT: GUSS, Bengt
APPLICANT: HOOK, Magnus
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: PATTI, Joseph
APPLICANT: SIGNAS, Christer
APPLICANT: SWITALSKI, Iech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESS: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-006

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1183 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-447-031A-2

Query Match 3.8%; Score 148; DB 2; Length 1183;  
Best Local Similarity 19.7%; Pred. No. 0.0022;

Matches 165; Conservative 123; Mismatches 299; Indels 252; Gaps 44;

64 POSSEYRWY---GYESVYRGHPYK-----QFVAHDLRVNLEGSRSY---OVYCF 109  
182 PEOITVHVRKFLNNKSKSYSDITIKDQIQGQQLDLSTLNINVTGTHSNYSGSALT 241  
110 NLKAPPLGS-----DSSVKRWYKKHKGISTKFEVYMSPRITG----- 148  
242 DFEKAPR-SSKITVDVTKMTIDVTIPQGYGSYNSFSINYK-----TKITNEQKFEVNS 295  
149 -----DELNOKLRAYVNGHPONANGIMG-----LEPLNATRVQEAVMYSDNA 194  
296 QAWYQEHKGEVNGK--SENHTVHNINANAGIEGVKGLKVLKQDKDK-----A 344  
195 PISNPDESFK-RESESNLVSLSQSLMRQALQIDPNLATKMPKQVPPDFOLSFESF-- 252  
345 PIAN--VKRLSKKDSYVKDNO---KEIETITANGIANIKALPSGDYILKEIENAR 397  
253 ---DKGRY-----NKGYQNLISGL-----VPTKPPTPGDPMPPNQPTTSV 293  
398 PYTFDKDEYPTFKMDTNOGYFTTIEKNAKIEKTKDVSQKWEQTKVKP-----TI 451  
294 LIRKVAIGYS-----KLEBQATLQITGDVNSVQARVSSND-IGETIELSDGT 342  
452 YEFKLYKODNQTTPVDKAEIKKLEGGTKVWSNL-----PNDKKGAIAK----- 498  
343 YLTLELN-----SPAGYSIAE-----PI-TFKVAGKVTYLLIDGKOLENNKEI 385  
499 YLVKEVNAGCEEDTPREGYTKKENGVLVNTKEKIEFTSISGEVMDKDNQDKRBEK-- 556  
386 VEPYSVEAYNDEESVSLTQNYAKFY---AKNKNSSQVYVCEFNADLKSPPSEDO 440  
557 ---VSYNLLANGEKVKTLDVTSNNKYEKDLPKYDEG-KKIEYTVTEBDHYKDYTTDIN 612  
441 GKMTPTDFTTGEKVTYHNGRLDFKTYVPRDTPDTPLKHIKKIVLEK----- 488  
613 GTTITTKYTPGETSATVTKNMDNNNODGKRPEIKVELLYODGKATGTAALINESNNMTH 672  
489 ---GYREKQAIIEYSGLETOLRAATQ-----LAIYFTDSAEIDKDLKDY 532  
673 TWTGDEKAKAGQGVKTYVELTKYKGYTHVDNNDMGNLVTNKKYTPETTSISGEKVM- 731  
533 HGFQDNDSSTLAVAKTIVEAODSNPQTLDDFLIPNNKKYQSL---IGTQHPREDVD 589  
732 ---DKDN-----ODGKRPEKYSVN-LLADEKVKTLDTVSTNNKYE-FKD 772  
590 IIRMEKKKVIPTNHLTLKRYTGLAGRTQDFHEIFE-----LKNNOELLSSQVKT- 643  
773 LRPYDGGKKI-----EYVTV---EDHVADYTTDINGTTITNNKYTPGETSATVTKM 820  
644 -DKTNLE-----FKDGKAT-----INLKGESELTLOGLP-----GYSYLK- 680  
821 DDMNNDGKRPEIKVELYQDGKATGKTALINSNMTHTWGLDKAKAGQGVKTYVEL 880  
681 TQSEGYKAVNSQEVANATVSK-----TGTSDETLAEENKREPVPGVDOKI--NG 731  
881 TKVGYTTHVDNNDMGNLVTNKKYTPETTSISGEKVMDDKDNQDKRPEKYSVNLANG 939

## RESULT 6

US-08-714-402-2

; Sequence 2, Application US/08714402

; Patent No. 5910441

; GENERAL INFORMATION:

; APPLICANT: ROCHA, Claudia

; TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESS: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,402

; FILING DATE: 16-SEP-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 016921-097

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1112 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-714-402-2

Query Match 3.7%; Score 145; DB 2; Length 1112;  
Best Local Similarity 19.8%; Pred. No. 0.0035;

Matches 190; Conservative 121; Mismatches 327; Indels 324; Gaps 51;

21 KNSKRTVTLV--GVFLMI-----FALVTSVYKATVFGLVESSTPNAINPDSSSEYRW-- 72  
112 KTSRTVTVTVYENGYTKKLVENPYNGELISAGSKDV-----SSLDLENKKMSVSKYK 166  
73 ---GYESYVRGHPY---KQ-----FVAHDLRVNLEGSRSYOVYCF 109  
167 TEVSSAADFYRNHNAVYFKMSFELKQDKSETINPGDTFVLQDRRLNRG----- 217  
110 NLKAPR-----LGSDDSYKKYKKHKGISTKFEVYA----- 141  
218 -ISODIPKIIYDSANSPILAIGKYHAENHOLIYFTFTYIAGLDKVLQSAETSLFLENKEV 276  
142 ---MSPRITGDELNOK--LRAYVNGHPONANGIMEGL-----EPLNAIVTQE 185  
277 EMTSINFKSTIGGOETTYKGTAVNLVGNESIKESNITINGLSNVGGSIESYNT--ETGE 334  
186 AWVYSDNAPISN-PDESFK-----RESESNLVSLSQSLMRQALQIDPNLATKMP 237  
335 FVWYVYVNPRTNIPATNMLMGFGARASNTSDLENDAMTSSALEIDYEVPEBEKLP 394  
238 KOVPD-----FOLSFESDEKDK-YNKGY----- 262  
395 SSYGVVTVTKLITFTDITAGLGNQFMTKQRIDFGNNIONKAFIIVTGTQDSGKPLV 454  
263 -QNLIS-----GG-----LVPTKPPTPGDPMPPNQPTTSVILRKYA 299

DB 455 QSNLASFRGASEYAAFTPVGNGVYFONEIALSPKSGSGSKSEF--TKPSIYVANKLRVA 512  
QY 300 IDGYSKL-----LEGATLQTLGDVNSFOARVESNDIGE--RIELSPGTYTLFELNSP 351  
DB 513 QLRFKMSTIDNPLPPAELALSSNGNS-QKLEASSNTGVEHFMDLISGTYIDLYTKAP 571  
QY 352 AGYS-----IAEPIF-----KVEAGKYTIIDGKO-IENPNKEIVE 387  
DB 572 KGYYQVTEKLAVTVDTTPRAEEMVTWSPHSSVYKVEANNEVTIVHKEETLFPSSKIME 631  
QY 388 PYSVEAYNDPEEFVLTTONYAKFYAKKNGSSQVYCFNADLKSPPSDEGCKMTPD 447  
DB 632 -----NDRPD-----ORPAKIYQLLQNGQ-----KMPNOIOE-----VTRKD 663  
QY 448 FTTGVEKYTHINGROLFKYTVKPRDTPDPTPLKHKKVLEKGRGQALEXSGLETQD 507  
DB 664 ---NDWSY-HF--KDLPKYDAKMOE-----YKSYVEAVNPBGYVSYLGDIFNT 708  
QY 508 RAATQALAIYFTDSAEIDKLDYHFGDMNDSTLAVAKLIVEYQDS--NPPQLTDD 565  
DB 709 R-ETEFVFPQNNFNLEFGNAEIKGSGSKIIDEDTLTSFKKKIMKNDPAENRQALQYQ 767  
QY 566 FF-----INNNKYOSLITQWHP-----DLV-----D 589  
DB 768 LYADGVAVEGQTFKISGSGNEMSFEEKNLKKYNGTGNDIIVSYKEVTVPTGYDVYSAND 827  
QY 590 IIRMEDEKKEVI-----PYTNHLTKRTVTVGLAGDRTKDFHEIE---LKNKKOELLS 638  
DB 828 IIR-NTKREVITYOQCKLEIEETLPLESGASG--GTTVEDSRPVTLSGLSSEQOSGD 883  
QY 639 QTVKTDK-TNLEEK---DGK---ATINLKHESSLTLOG-----LPEGYSYL 677  
DB 884 MTLIEDSATHIKFSKRDIDQKELAGATMELRDSGKTIPTWISDGQVNDLYMPGYTF- 942  
QY 678 VETSESGKV-----KNSQEVANATYSKIGTITSEDLAFENKEPVPTG---VDQ 727  
DB 943 VETAAPDGIEITATITFTVNEQ--GOVTYNGKATKGDTHVMADKPTKSGQVIDIEB 1000  
QY 728 KI 729  
DB 1001 KI 1002

RESULT 7  
US-08-703-947-2  
Sequence 2, Application US/08703947  
Patent No. 5788962  
GENERAL INFORMATION:  
APPLICANT: Wise, Kim S.  
TITLE OF INVENTION: DNA Sequences Coding for Mycoplasma  
TITLE OF INVENTION: Hypopneumoniae Surface Antigens,  
TITLE OF INVENTION: Corresponding Proteins and Use in  
TITLE OF INVENTION: Vaccines and Diagnostic Procedures  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Grace J. Fishel  
STREET: 929 Fee Fee Road, Suite 100  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63043  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage  
COMPUTER: Hewlett-Packard Vectra 3.3  
OPERATING SYSTEM: MS-DOS Version 5.1  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,947  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,957

FILING DATE: January 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fishel, Grace J.  
REGISTRATION NUMBER: 25864  
REFERENCE/DOCKET NUMBER: UYA 8141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 878-0440  
TELEFAX: (314) 275-7693  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 amino acid residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Predicted amino acid sequence of complete  
DESCRIPTION: 627 residues of the P65 lipoprotein, derived  
DESCRIPTION: from the nucleic acid sequence  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE: whole polypeptide  
ORIGINAL SOURCE:  
ORGANISM: Mycoplasma hypopneumoniae  
STRAIN: J  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: unicellular bacterium  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY: Genomic in Charon 4A, GEM12  
CLONE: MhpJ25, MhpJ35, MhpJG35, PzJ25, PzJ25.14,  
CLONE: PzJG35.1, PzJG35.12, PzJG35.13, PzJG35.14  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: single chromosome  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: 627 amino acid sequence representing  
NAME/KEY: complete sequence (including signal  
NAME/KEY: sequence) of surface lipoprotein P65  
LOCATION: entire derived coded sequence  
IDENTIFICATION METHOD: clone identified by immunodetection of  
IDENTIFICATION METHOD: protein product with antiserum specific for  
IDENTIFICATION METHOD: P65; residue sequence deduced from nucleic  
IDENTIFICATION METHOD: acid sequence  
OTHER INFORMATION: Immunogenic surface lipoprotein of no known  
OTHER INFORMATION: function; C-terminus exposed on external  
OTHER INFORMATION: surface of cell; N-terminal signal sequence  
OTHER INFORMATION: (first 29 amino acid residues) cleaved during  
OTHER INFORMATION: lipid modification process  
PUBLICATION INFORMATION:  
AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J.  
AUTHORS: Stull, Mark A. McIntosh, and Kim S. Wise  
TITLE: Identification and Mapping of an  
TITLE: Immunogenic Region of Mycoplasma  
TITLE: hypopneumoniae p65 Surface Lipoprotein  
TITLE: Expressed in Escherichia coli from a Cloned  
TITLE: Genomic Fragment  
JOURNAL: Infection and Immunity  
VOLUME: 58  
ISSUE: 8  
PAGES: 2637-2643  
DATE: August 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 627  
US-08-703-947-2



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Db 1817 -----SLYNEKFYINNEGMVSG--LIYINDSLYEFKPPV--NNLITGFVVGDDKYY 1865
QY 345 LTELNSPAGSIAPSI-----TFKVEAGKY-----TI-----IDKQIE 379
Db 1866 FNPINGAA-SIGETIIDKNYFNOSGVLTQVFTSEDFKIFAPANTIDENLEGAID 1924
QY 380 NPNKEIVER--YSVEAYNDFEESVLTQNVAKFYA-----KKNKSSQVVCENA 429
Db 1925 FTGKLIIDENIYFDDNRYGAVEMKELDGMH--YFSPETGAKFGLNIGDYKYYFNS 1981
QY 430 D--LKSPDSEDEGKMTPTFTTGEVAKYTHIAGR-----DLFKYTVK 469
Db 1982 DGVMQKGFVSINNKHFVDSGVAKGYTEIDGKHFFAENGEMOIGVFTEDEGFKY-- 2038
QY 470 PRDTPDTFLKHKKVLEKGYREKGAIEYSGLTETQLRAATOLAIYFETDSAE----- 523
Db 2039 -----FAHNHEDL-----GNEGEETISYGLINFNNK-----IYFDSTFVAVGWK 2080
QY 524 -----LDKDKLNDYHGFQDMN-----DSTLAVAKLIVE----- 551
Db 2081 DLBDGSKYVDEDETAELAYIGLSLINDGOYFENDGIMQVGFVINDKVFYFSDSGIIESG 2140
QY 552 -----YAQDSNPPQLTDL-----FFIFNNN-----KYQSL----- 577
Db 2141 VQNIIDNIFYIDNGIYQIGVFPTSDGYKFAFAPANTVNDNIYQAVESGLVAVGEDVYY 2200
QY 578 -----IGTQWHPEDLVDIIRMEDKKEVIVPTNHLIRKVTGLAGRTDFHFE----- 626
Db 2201 FGETYITETGW-----IYDMENESDKYFENPET-----KKACKGINLIDDIKYYFDEKGIN 2251
QY 627 -----IELKNNKQELLQSOTVTKTNLEFKDKATINLK-----HGESLTLQ-----GLPEGYS 675
Db 2252 RUGLISENNNYF-----NENGMQFGYINIEDKMYFPEBDGVMQIGVNTPTDGFK 2303
QY 676 YLYKE 680
Db 2304 YFAHQ 2308

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; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: INGOLTA, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPD-01308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-405-496A-10

Query Match 3.5%; Score 139; DB 2; Length 2366;
Best Local Similarity 19.6%; Pred. No. 0.036;
Matches 154; Conservative 86; Mismatches 249; Indels 296; Gaps 38;

QY 83 PYKQKPRVAH-----DLRVNLEGSRSYQYVCFNLKKAFLPGSDSSVKKWT 127
Db 1633 PYFKFNTLETNTLYLVGNRQNMIVPENYDLDDSGDISSTVINFESQKYLVDIGDSYCNK-- 1690
QY 128 KKHGDISTKREDYAMSPRITGDELNOKLRAMVYNGHQ-----NANQIMESLEPLNIRVY 183
Db 1691 -----VVISPNTYTDINTPYETENNTPEVIVLDANIYENKIN--VNINDLS 1737
QY 184 QEAWYYSNAPISNPDESFKRESNLTSTSLMRQALKOLI-----DPNLATFMPKQ 239
Db 1738 IRYVW-----SNDGNP-----ILMSTSEBNKVSQKIFVAVFKDKTLANKLS-- 1781
QY 240 VPDDFQLSIFSEDEKGD-----KYNKGYONLSG-----GLVPTKPPTPGPPMD 284
Db 1782 -----FNFSDKQDVPEYSEIILSFTPSY-----YEDGLIGYDLGLV----- 1816
QY 285 PNOPTTSVILIRKAYIGDYKLLLEGATLQLTGDNVNSFOARVSSNDIGRIELSDGTYT 344
Db 1817 -----SLYNEKFYINNEGMVSG--LIYINDSLYEFKPPV--NNLITGFVVGDDKYY 1865
QY 345 LTELNSPAGSIAPSI-----TFKVEAGKY-----TI-----IDKQIE 379
Db 1866 FNPINGAA-SIGETIIDKNYFNOSGVLTQVFTSEDFKIFAPANTIDENLEGAID 1924
QY 380 NPNKEIVER--YSVEAYNDFEESVLTQNVAKFYA-----KKNKSSQVVCENA 429
Db 1925 FTGKLIIDENIYFDDNRYGAVEMKELDGMH--YFSPETGAKFGLNIGDYKYYFNS 1981
QY 430 D--LKSPDSEDEGKMTPTFTTGEVAKYTHIAGR-----DLFKYTVK 469
Db 1982 DGVMQKGFVSINNKHFVDSGVAKGYTEIDGKHFFAENGEMOIGVFTEDEGFKY-- 2038
QY 470 PRDTPDTFLKHKKVLEKGYREKGAIEYSGLTETQLRAATOLAIYFETDSAE----- 523
Db 2039 -----FAHNHEDL-----GNEGEETISYGLINFNNK-----IYFDSTFVAVGWK 2080
QY 524 -----LDKDKLNDYHGFQDMN-----DSTLAVAKLIVE----- 551
Db 2081 DLBDGSKYVDEDETAELAYIGLSLINDGOYFENDGIMQVGFVINDKVFYFSDSGIIESG 2140
QY 552 -----YAQDSNPPQLTDL-----FFIFNNN-----KYQSL----- 577
Db 2141 VQNIIDNIFYIDNGIYQIGVFPTSDGYKFAFAPANTVNDNIYQAVESGLVAVGEDVYY 2200
QY 578 -----IGTQWHPEDLVDIIRMEDKKEVIVPTNHLIRKVTGLAGRTDFHFE----- 626
Db 2201 FGETYITETGW-----IYDMENESDKYFENPET-----KKACKGINLIDDIKYYFDEKGIN 2251
QY 627 -----IELKNNKQELLQSOTVTKTNLEFKDKATINLK-----HGESLTLQ-----GLPEGYS 675

```





```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 567-2020
: TELEFAX: (215) 567-2991
:
: TELEEX: 831-484
:
: INFORMATION FOR SEQ ID NO: 4:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 1861 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS:
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: OS-08-790-912-4

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Query Match	3.4%	Score 134	DB 2	Length 1861
Best Local Similarity	18.0%	Pred. No.	0.064	
Matches 135	Conservative 117	Mismatches 242	Indels 258	Gaps 33

QY	19	LSKNSKRETVLIVGVFLMIFLFAVYSMGAKTVFGLVESPFLNALINPOSSSEYRWYGESEY	78
Db	659	LAKKAEREVYTFEFSNULVQAINNNNG--TYLLASLANANEVLEN-----GASST	70857
QY	79	VRGHPHYKQFVVAHDLRVNLGSSRSYOVCEYCNLK-AFPLGSDSSVAKWYKKHDIISTKF	137
Db	709	IKGFRFTGKLF-----GSKDKGNVAITY--NLKKPLFDLSAATVENLTLDKDVNSGKT	756
QY	138	EDYAMSPRITDDELNOKLRAVMYNGHONANGMEGLEPLMLAIRVTOBAAVWYSIDNAPIS	197
Db	759	DIGALA-----NEANMATR--INNVH--VDGVLAGERGJGL-----WV-KADNSKIS	801
QY	198	NPDESFKRESESNIVSTQSLSIMRQALCOLIDPMLATIKMPQOVDPDQOLSFISESDGDK	257
Db	802	N--SSFK-----GRIVNSE-----IKAP-----	818
QY	258	YNKGYONLLSGVLVPTKPPPGDEPMPNPOTTSVLIRKAYIGDYSKLLEGATLOLTD	317
Db	819	YN-----IGGLV-----GQLGCI-----NALVDSK--ATITIS-S	846
QY	318	NVNSFOARVESNDIGERIELSDGTITILEINS-----PAGYSLAETITKVAAGK	366
Db	847	NADSTNQTUVGSLAGLEVKEDALISVSIEGINNNKRFGSVAGVAGYLMDRDSSEERHAGR	906
QY	369	VYTIIDKOIENPKMKEIPEYSAVYNDEEFESVLTTONAKFYAKNNKNGSSQVYVCFN	428
Db	907	LHNVLSDINWANGN-----AISYHTRGKRITDYS-----NKDR-----	942
QY	429	ADLSPDSEDGKTPMPTDFTTGVEKYYTHIAGRDLFKYTVKPRDTPDPTFLKHAKIYEK	488
Db	943	-----YVKVTLKEKDEV-----YTKE	957
QY	489	GYPEKGAIIEVSGL-----TETQOLAALQOLAIYTTSDSALDKDKLQDHYGFGMNDSTLA	544
Db	958	SLEBERGTLDVSOJASKSEINSLAPAVETILTSTNKESDFSKVDY-----	100
QY	545	VAKLIVEAODSNPOLTLDIEFFIPNNN-----KYSLI--GTOHMEHDLYDILIMEDKK	597
Db	1006	-----QASRLAKYNIKKILPFTYNKATVYKGNLVEDSTLYLEKEILISAAMKD--	105
QY	598	EVIEVTNHLTRKTVTGTGIAGDRTDQFHEIELKNNKOELLQTVKTKETNL--EKKDKAT	656
Db	1055	-----NEVITDIASHKEAANKLLIHYKHOSSEKDLTYQDSOFSKIAEYRVGDT--	110
QY	657	INLKHGSLTLQGLPEGYSLVYKETFDSGKYKVKVNSQEVANAVYKGTGTSDETL--AF	713
Db	1103	-----GLIYTPNOFLQNHSSIVNEVLPDLKAVDQSAIRHTIGLISGSVSLTELYLEQF	115
QY	714	ENKKEPVPT-----GYDQKQINGYL	733
Db	1158	AKTKRENANTLEKLISADAVYASEQINGYV	1189

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: Sequence 2, Application PC/TUS9510661A
: GENERAL INFORMATION:
: APPLICANT: Washington University, et al.
: TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: United States
: ZIP: 94111-4187
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/10661A
: FILING DATE: 16-AUG-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/296,791
: FILING DATE: 25-AUG-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Treacartin, Richard F.
: REGISTRATION NUMBER: 31,801
: REFERENCE/DOCKET NUMBER: FP-59941/RFT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELERX: 910 277299
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1394 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: PCT-US95-10661A-2

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Query Match	3.2%	Score	128;	DB	5;	Length	1394;
Best Local Similarity	19.0%;	Pred. No.	0.12;				
Matches	163;	Conservative	117;	Mismatches	281;	Indels	298;
						Gaps	43;

[illegible]

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QY 388 PSVGEAVNDEEFSVLTQYAKFYAKKNGSSQVYCCPNADLKSPDS--EDGCKTWT 445
DB 354 IYSPR-----LNNGETLYFMDQKGS-----LIFASDINOGAGLYEGNETVVS 397
QY 446 PDFT-TGEVAYTHIAGRDLFKYTVKPRDTPDPLK-----HI-----K 483
DB 398 PNEGOWMOGAGIHVSNS--TVTWKYNVGEHDLISKIGKGLHVAOKGKNGSISVGDCK 455
QY 484 KVIKGYREKGOAIEYSGLETOLRAATOLAIYFTDSAEIDKDKLDYHFGC---DMN 539
DB 456 VILEQOADDGNGKQAFSEIGELVSGRGTVQL-----NDDKQFDPKF--YFGFRGRLDLN 508
QY 540 DSHLAVALIVEADSNPPQLTDLDFEIPNNKXQSLIGTOMHPELV-----DIIRME 554
DB 509 GHSLETKRI-----QNTDEGAMIVNHTTQAAVNTTGNESIVLPNGNNINIKLD 557
QY 595 DKREVIPTVHTLRTKTVGLADRTKDFEIELEKNNKQELLSQTVKTKD-----TN 647
DB 558 YRKEI-----AYNGWFEETDKNKH-----NGRLNLTKPTTEDRTILLSGTN 600
QY 648 LE-----FKDKAT-----INLKHGESLTLOGLPEG-----YSYLVKETDSEGY 686
DB 601 LKGDITQTKGKLFPSGRPTPHAYVNLNKRWSE--MEGIPOGEIWDHDMINRTFKAENF 657
QY 687 KVVNNGEVA-----NATVSK-----TGITSDETLAEFN 716
DB 658 QINGGSAVVSRRVNSIEGMNTVSNANAFGVVPPNOONTICRSMDWTGLTTCOKVLDLTP 717
QY 717 KEVPVPTGVOKINGYLAL 735
DB 718 K--VINSIPKTOINGSINL 734

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RESULT 13
US-08-946-475-2
; Sequence 2, Application US/08946475
; Patent No. 6013505
; GENERAL INFORMATION:
; APPLICANT: Gwynn, Michael
; APPLICANT: Kallender, Howard
; APPLICANT: Palmer, Leslie
; TITLE OF INVENTION: TOPOLISOMERASE I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: PASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,475
; FILING DATE: 08-OCT-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/027,973
; FILING DATE: 08-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50560
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 691 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-475-2

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Query Match 3.2%; Score 125.5; DB 3; Length 691;
Best Local Similarity 19.8%; Pred. No. 0.066;
Matches 133; Conservative 89; Mismatches 228; Indels 221; Gaps 33;

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QY 112 KRAFLPGSSSVKWKYKHHGISTK--FEDYAMSPRTGELNOKLRAYVYNGHPONANG 169
DB 25 KKYKVIASMGHVADLPDSQGVDTEDNYEPKTYITIGKGVVLELK-----HAKKAK 78
QY 170 IMEGLEPLNAIRVTOEAWVYS-----DNAPISNP-----DESEFN--RESESNLV 212
DB 79 VFLASDP--DREGELAMHLSKILELEDSKENRVYFNETTKDAVSEFRNPREIEMNLV 135
QY 213 STQSLSMRQALKOLIDPNLATKPKOV-----PDE 244
DB 136 DAOQ--ARRILDRLVGYNISPVLMKKVKKGSAGRVSYALRLVIDRENEIRNFRPEEX 192
QY 245 QLSIFSEDKGDKYK--GYON-----LLSGGLVPTKPPPGDPMMP 285
DB 193 WTEGEPRIKSKFNAKFLHYKPKPKLTKKDYKETAALDSDQFEITVNTKKEKTRNP 252
QY 286 NOPOTTSVLIRKRYAIGDYSKLEGAFLQLTGDNVNSFOAR--VFSSNDIGERIEL--SDGT 342
DB 253 ANPFTS-----TLQDEARKLNFKAKTMMVAQOLYEGIDLKKOG 294
QY 343 YTL-----TELSNPAGYSIAEPTTFKVEAGKYTYI--IDGQIENPKELVEPY 390
DB 295 IGLITYMRTDSTRISPTAKAKAOYITDKY--GESYTSKRKASGKODDPAHEAIRPSSP 352
QY 391 VEAVNDEEFSVLTQNYAFYAKKNGSSQVYCCPNADLKSPDSECGKTMFDPT 450
DB 353 WRPDDMKSF--LTQOYRIYKLIWERFVASOMA-----PALLD--TVSLDITO 397
QY 451 GEVAYTHIAGRDLFKYTVKPRDTPDPLKIKKIVIEKGYREKGOAIEYSGLETOLRAA 510
DB 398 GDILK-----FRANGQIKKFGF----- 414
QY 511 TOLAIYFT--DSAEIDKD---KLKDYHGFQDMNDSTLAVAKLIVEAQ--DSNPQOLD 563
DB 415 --MTLYVETKDDSDSEKKNLPKLEQ---GD-----KVTAQIHPAQHYTQPPRYTE 462
QY 564 L-----DFEIP-----NNKXQSLIGTOMHPELVDIIRMEDK---EVP 601
DB 463 ARLVKTLEELKIGRSTYATPTDITOKRNVKLESKRFPVTEGELYVHEQVKEPPEIID 522
QY 602 VTHNLTLRTKTVGLA--GDRTKDFEIELEKNNKQELLSQTVKDKDNLKEDKATINLK 660
DB 523 VEFTVMMETLDDKIAAGDITWRKVIDGFSSFKQDY--EBAEEMKIELKDPA----- 575
QY 661 HGESLTLOGLP 671
DB 576 GEDCEVCGSP 585

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RESULT 14
US-08-946-475-9
; Sequence 9, Application US/08946475
; Patent No. 6013505
; GENERAL INFORMATION:
; APPLICANT: Gwynn, Michael
; APPLICANT: Kallender, Howard
; APPLICANT: Palmer, Leslie
; TITLE OF INVENTION: TOPOLISOMERASE I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation

```



```

Dб 194 EYTSQEI-----QMKTAT--EAFMETIKIEECS 223
Oy 476 DTEKHKUYEKYERKESQAIETSGTEQLAPATOLAITYTDSALDEKDKLYDNE 555
Dб 224 HTOCHSKDYIER--FREGEKEKETERIM-----NMUDKLS--RU 260
Oy 536 GDMDSLTAAKILVEVAOOSNPQLDLDPELIPNNKXYSGLGTOMHREDLVIITMED 595
Dб 261 GEHDSKRLREODLKKRALLDNR-----ETD-----KKNMST-----KDLIQLKKIRD 303
Oy 596 KKEVYPTVHNLTERTVYTAGDRTKDNFHELEKNNKOKELLSQTVKTDXTNLEFYGKA 655
Dб 304 -QHLVWLNHR-----GVRQRFLNAMLGIKNEKDSO--ESGYFIEEDENPNRYDEKT 350
Oy 656 -----TINLKHGESLTLOGLEPGYSYLVKEDNSG--KVVKVNSQ--EVANAPVSKT 703
Dб 351 WEVVDINRWQAEEL-LYKAKPDG--AFLIRRESKKGCYACSVVAOGEVKNHCYIYST 402

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